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Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2009; month=9; day=21; hr=11; min=11; sec=59; ms=20;]
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****
Reviewer Comments:
<150> 10/509,249
<151> 2004-09-28

Please remove these lines, since they are not prior application data.

<210> 30
<211> 39
<212> DNA
<213> artificial synthesized peptide sequence

<220>
<223> test fused

<400> 30

The above <213> response is invalid, per 1.823 of the Sequence Rules. The only valid responses are: the Genus species of the organism, "Artificial Sequence", or "Unknown". "Artificial Sequence" and "Unknown" require explanation in the <220>-<223> section; please clearly give the source of the genetic material. FYI: this is not a peptide sequence. Same error in Sequence 31.

Please ensure that all explanations of "Artificial Sequence" give the source of the genetic material.
****

Validated By CRFValidator v 1.0.3

Application No: 10509249 Version No: 6.0

Input Set:

Output Set:

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Finished: 2009-09-03 15:42:22.674
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 335 ms
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Total Errors: 0
No. of SeqIDs Defined: 245
Actual SeqID Count: 245

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W	213	Artificial or Unknown found in <213> in SEQ ID (19)
W	213	Artificial or Unknown found in <213> in SEQ ID (20)

Input Set:

Output Set:

Started: 2009-09-03 15:42:15.339
Finished: 2009-09-03 15:42:22.674
Elapsed: 0 hr(s) 0 min(s) 7 sec(s) 335 ms
Total Warnings: 245
Total Errors: 0
No. of SeqIDs Defined: 245
Actual SeqID Count: 245

Error code	Error Description
	This error has occured more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (31)

SEQUENCE LISTING

<110> Japan Science and Technology Agency
Kuroda, Shunichi
Tanizawa, Katsuyuki
Okajima, Toshihide
Kondo, Akihiko
Ueda, Nasakazu
Seno, Masahura

<120> THERAPEUTIC DRUG USING ANTIBODY-DISPLAYING HOLLOW PROTEIN NANOPARTICLES AND HOLLOW PROTEIN NANOPARTICLES

<130> 12480-000067/US

<140> 10509249
<141> 2004-09-28

<150> 10/509,249
<151> 2004-09-28

<160> 245

<170> PatentIn version 3.4

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<210> 28
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<212> PRT
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<400> 29

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Leu His Leu Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln
20 25 30

Ser Leu Lys Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala
35 40 45

Lys Lys Leu Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn
50 55 60

Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu
65 70 75 80

Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro
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Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala
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Gln Ala Pro Lys
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<220>
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<210> 31
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<213> Artificial Sequence Fused Peptide

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<223> 21-153 + ZZ (serotype y) sequence

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<213> artificial sequence

<220>
<223> protein corresonding to 21-153 + ZZ (serotype y) sequence

<400> 32

Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
50 55 60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu

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Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
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Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
        115                 120                 125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro
    130                 135                 140

Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145                 150                 155                 160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
                165                 170                 175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
            180                 185                 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
        195                 200                 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
    210                 215                 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225                 230                 235                 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
                245                 250                 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
            260                 265                 270

Cys Lys Thr Cys Thr Ile Pro Ala Gln Gly Thr Ser Met Phe Pro Ser
        275                 280                 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
    290                 295                 300
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Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
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Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
                325                 330                 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
            340                 345                 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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<220>
<223> 21-153 (Q129R) + ZZ (serotype y) sequence

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caaagtttaa aagatgaccc aagccaaagc gctaaccttt tagcagaagc taaaaagcta    240

aatgatgctc aggcgccgaa agtagacaac aaattcaaca aagaacaaca aaacgcgttc    300

tatgagatct tacatttacc taacttaaac gaagaacaac gaaacgcctt catccaaagt    360

ttaaaagatg acccaagcca aagcgctaac cttttagcag aagctaaaaa gctaaatgat    420

gctcaggcgc cgaaagcggc cgcccctgca ccgaacatgg agaacacaac atcaggattc    480

ctaggacccc tgctcgtgtt acaggcgggg tttttcttgt tgacaagaat cctcacaata    540

ccacagagtc tagactcgtg gtggacttct ctcaattttc tagggggagc acccacgtgt    600

cctggccaaa attcgcagtc cccaacctcc aatcactcac caacctcttg tcctccaatt    660

tgtcctggct atcgctggat gtgtctgcgg cgttttatca tattcctctt catcctgctg    720

ctatgcctca tcttcttgtt ggttcttctg gactaccaag gtatgttgcc cgtttgtcct    780
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cgaggaacct ctatgtttcc ctcttgttgc tgtacaaaac cttcggacgg aaactgcact 900

tgtattccca tcccatcatc ctgggctttc gcaagattcc tatgggagtg ggcctcagtc 960

cgtttctcct ggctcagttt actagtgcca tttgttcagt ggttcgtagg gctttccccc 1020

actgtttggc tttcagttat atggatgatg tggtattggg ggccaagtct gtacaacatc 1080

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<213> artificial sequence

<220>
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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20 25 30

Lys Phe Asn Lys Glu Gln Gln Asn Ala Phe Tyr Glu Ile Leu His Leu
35 40 45

Pro Asn Leu Asn Glu Glu Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys
50 55 60

Asp Asp Pro Ser Gln Ser Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu
65 70 75 80

Asn Asp Ala Gln Ala Pro Lys Val Asp Asn Lys Phe Asn Lys Glu Gln
85 90 95

Gln Asn Ala Phe Tyr Glu Ile Leu His Leu Pro Asn Leu Asn Glu Glu
100 105 110

Gln Arg Asn Ala Phe Ile Gln Ser Leu Lys Asp Asp Pro Ser Gln Ser
115 120 125

Ala Asn Leu Leu Ala Glu Ala Lys Lys Leu Asn Asp Ala Gln Ala Pro

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Lys Ala Ala Ala Pro Ala Pro Asn Met Glu Asn Thr Thr Ser Gly Phe
145                 150                 155                 160

Leu Gly Pro Leu Leu Val Leu Gln Ala Gly Phe Phe Leu Leu Thr Arg
                165                 170                 175

Ile Leu Thr Ile Pro Gln Ser Leu Asp Ser Trp Trp Thr Ser Leu Asn
            180                 185                 190

Phe Leu Gly Gly Ala Pro Thr Cys Pro Gly Gln Asn Ser Gln Ser Pro
        195                 200                 205

Thr Ser Asn His Ser Pro Thr Ser Cys Pro Pro Ile Cys Pro Gly Tyr
    210                 215                 220

Arg Trp Met Cys Leu Arg Arg Phe Ile Ile Phe Leu Phe Ile Leu Leu
225                 230                 235                 240

Leu Cys Leu Ile Phe Leu Leu Val Leu Leu Asp Tyr Gln Gly Met Leu
                245                 250                 255

Pro Val Cys Pro Leu Leu Pro Gly Thr Ser Thr Thr Ser Thr Gly Pro
            260                 265                 270

Cys Lys Thr Cys Thr Ile Pro Ala Arg Gly Thr Ser Met Phe Pro Ser
        275                 280                 285

Cys Cys Cys Thr Lys Pro Ser Asp Gly Asn Cys Thr Cys Ile Pro Ile
    290                 295                 300

Pro Ser Ser Trp Ala Phe Ala Arg Phe Leu Trp Glu Trp Ala Ser Val
305                 310                 315                 320

Arg Phe Ser Trp Leu Ser Leu Leu Val Pro Phe Val Gln Trp Phe Val
                325                 330                 335

Gly Leu Ser Pro Thr Val Trp Leu Ser Val Ile Trp Met Met Trp Tyr
            340                 345                 350

Trp Gly Pro Ser Leu Tyr Asn Ile Leu Ser Pro Phe Leu Pro Leu Leu
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gcgttctatg agatcttaca tttacctaac ttaaacgaag aacaacgaaa cgccttcatc 180

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<210> 36
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sequence

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Met Gly Thr Asn Leu Ser Val Pro Asn Pro Leu Gly Phe Phe Pro Asp
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His Gln Leu Asp Gly Gly Arg Ala Gln His Asp Glu Ala Val Asp Asn
20